



Integration of data and model in cardiac electrophysiology

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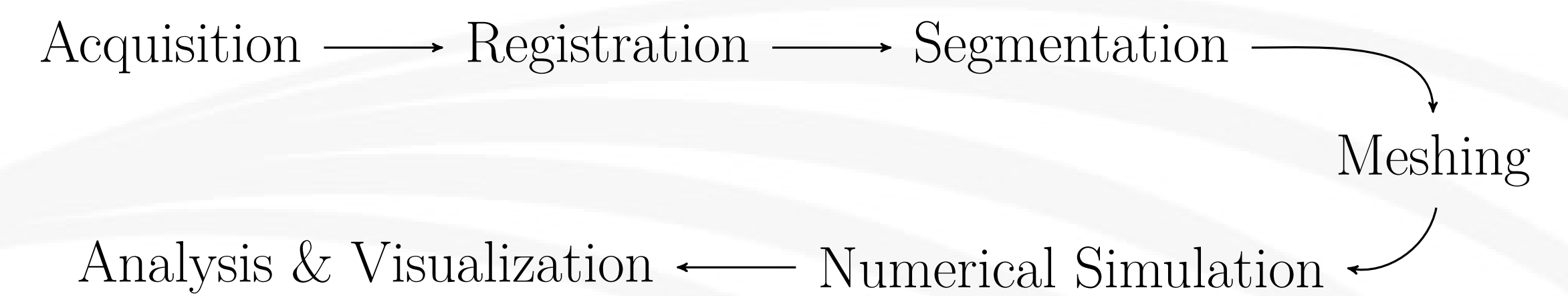
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Introduction

Carmen team aims to build complete realistic models of the electrical activity of the heart. The study of such models is a multistep process, which can be summarized by 3 main steps:

- preprocessing phase to obtain meshes and parameters from imaging and experimental data
- use a numerical simulator to solve cardiac electrophysiological models
- postprocessing phase to visualize, analyze and confront results to reality



Motivation

On the one hand, building complex anatomical meshes raises **major issues**:

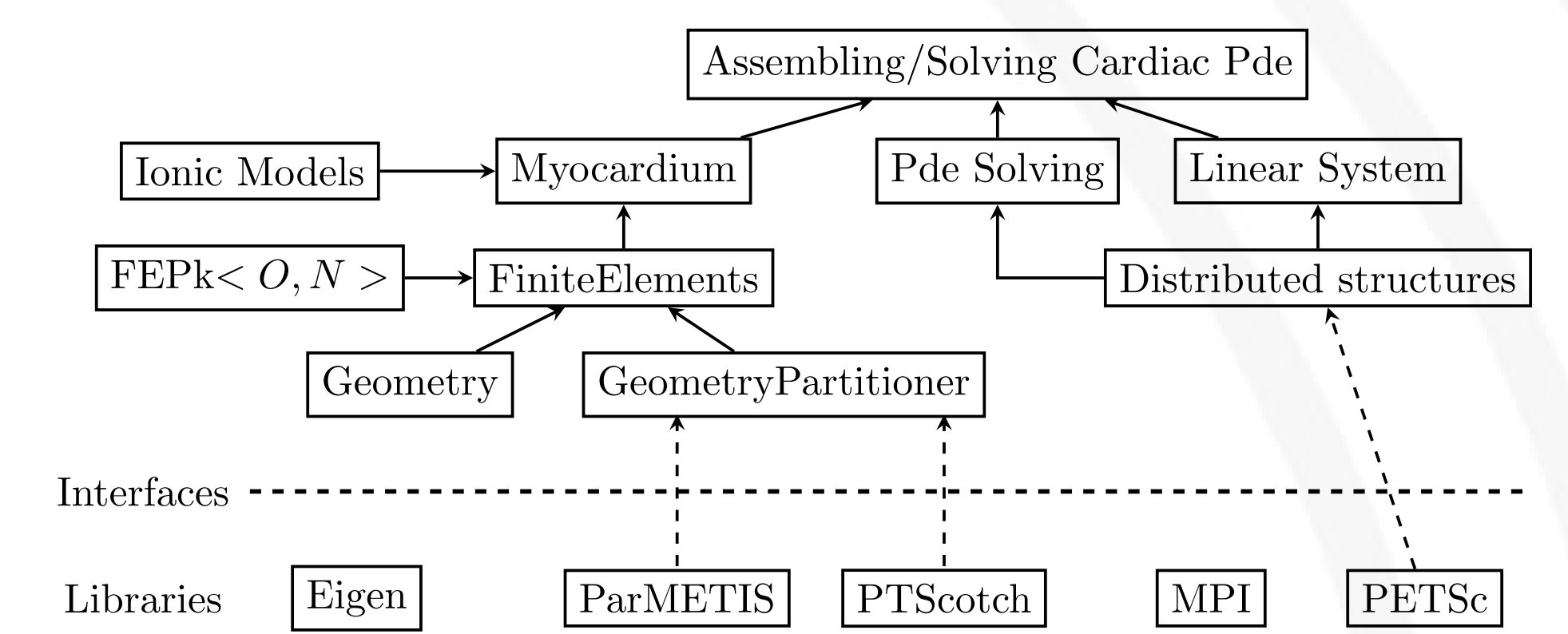
- time-consuming
- error-prone
- specific expertise needed
- require multiple softwares

On the other hand, the computing time for numerical simulation is proportional to the complexity of the model and the size of the domain.

Main goal: **streamline** all the workflow from preprocessing to postprocessing in the MUSIC environment.

The Cardiac ElectroPhysiology Simulator aims to integrate a broad range of multiscale models, and to make use of computing capacity of clusters. It features:

- finite elements P1/P2
- simple or bilayer monodomain model
- multidimensional meshes (1D/2D/3D)
- supported I/O formats: VTK, Medit and Tetgen
- hard-coded ionic models: TTNP, CRN, MS, BR
- multistep time integration schemes : Rush-Larsen , SBDF
- parameters file with simple syntax
- distributed memory parallelism : MPI and PETSc
- programmed in C++11 with templates and dynamical polymorphism



Overview of the module organization in CEPS

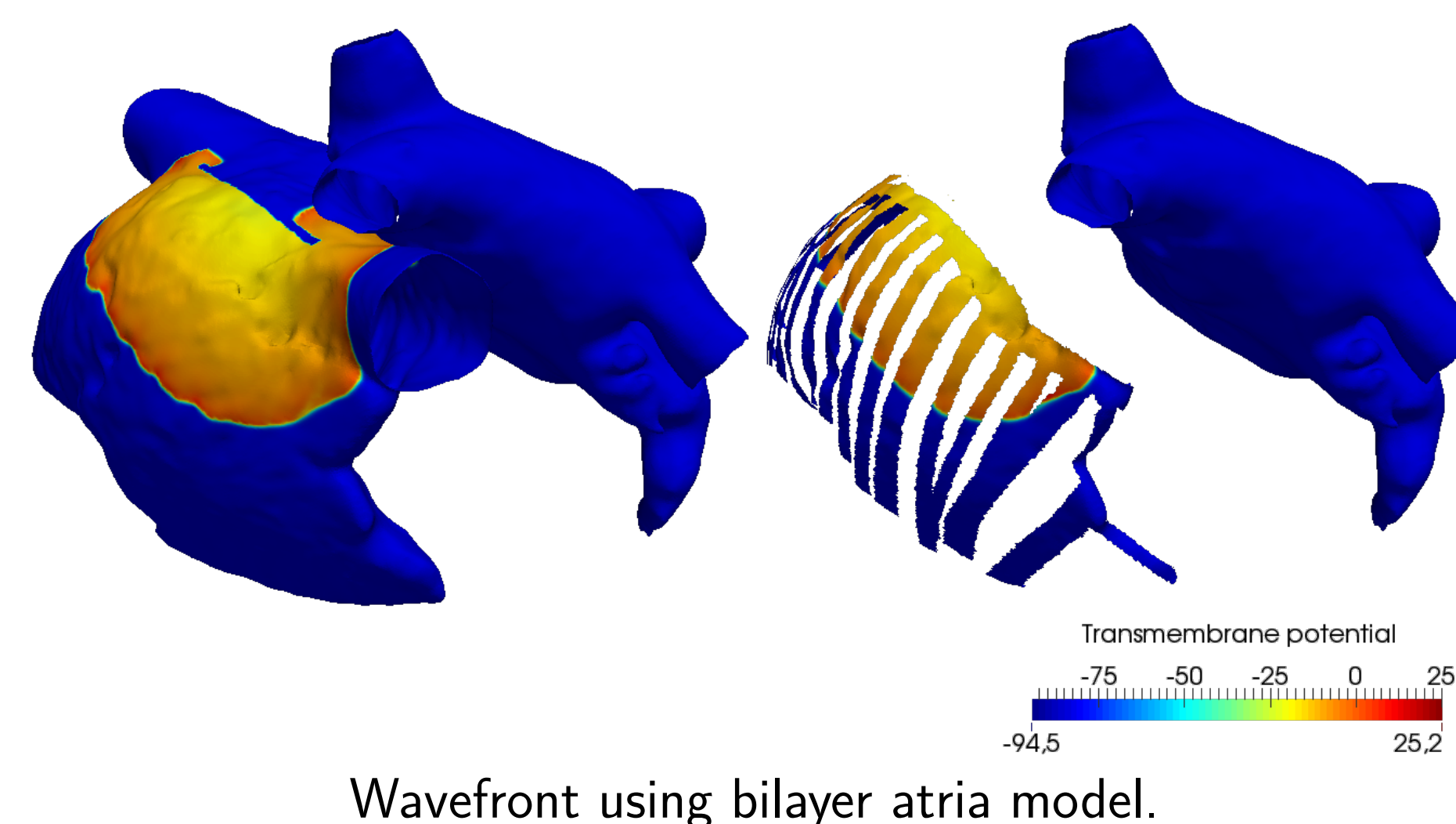
MULTI-modality platform for Specific Imaging in Cardiology

MUSIC is a joint *Liryc* and *Inria* platform used to visualize and process cardiac imaging and electrical data.

- toolboxes organized in workspaces for image and surface mesh processing
- pipeline architecture, a step-by-step approach for a given problem



Our aim: **expand** the possibilities of MUSIC by adding toolboxes and implementing specialized pipelines.



Wavefront using bilayer atria model.

The monodomain model

The monodomain model describes the evolution of the transmembrane potential V_m in myocardial tissue Ω .

$$\begin{aligned} \chi(C_m \partial_t V_m + I_{ion}(V_m, w)) &= \text{div}(\sigma \nabla V_m) + I_{app} & \text{on } \Omega \\ \partial_t w + g(V_m, w) &= 0 & \text{on } \Omega \\ (\sigma \nabla V_m) \cdot n &= 0 & \text{on } \partial\Omega \end{aligned}$$

Toolbox examples

Utility tools on meshes

Regroups common operations on meshes

- append, clean, merge
- conformity and manifoldness
- hole detection
- quality metrics



Imaging:

- CT-scan or MRI
- segmentation step, creates masks:
 - torso
 - lungs
 - rib-cage
 - pericardium
- mask filtering

Meshing:

- associate masks with regions
- volumic meshing using multiple constraints
- verify conformity and quality

Simulation:

- generate input file with simulation parameters
- launch numerical simulation process on cluster

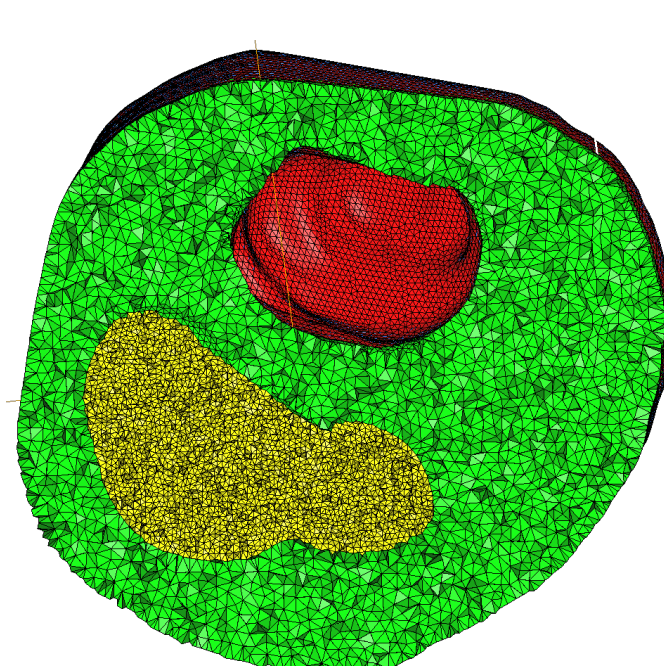
Postprocessing:

- import results
- visualization and analysis

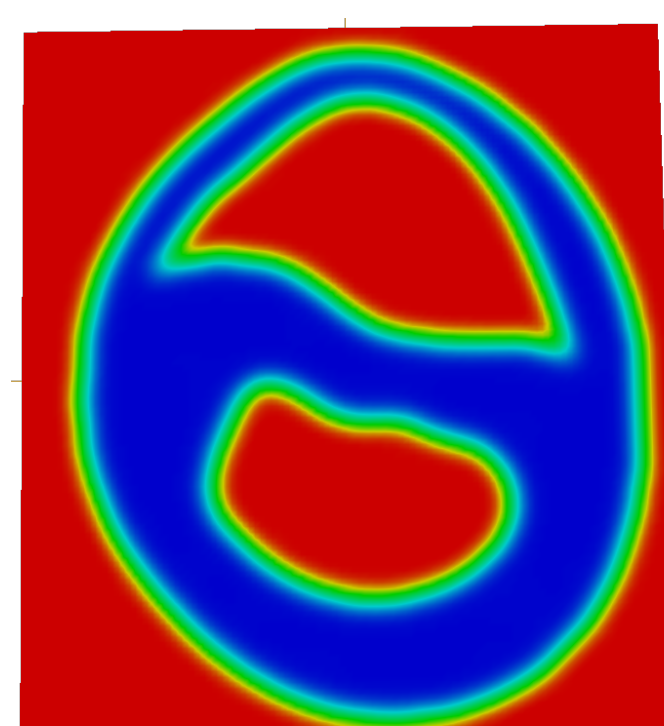
Volume and surface meshing

Specialized libraries to generate high quality meshes.

- Tetgen: volumic meshing from piecewise linear complex. Able to specify holes inside the volume
- MMG suite: implicit domain meshing, surface and volume remeshing



Tetgen generated mesh with different volume constraints.

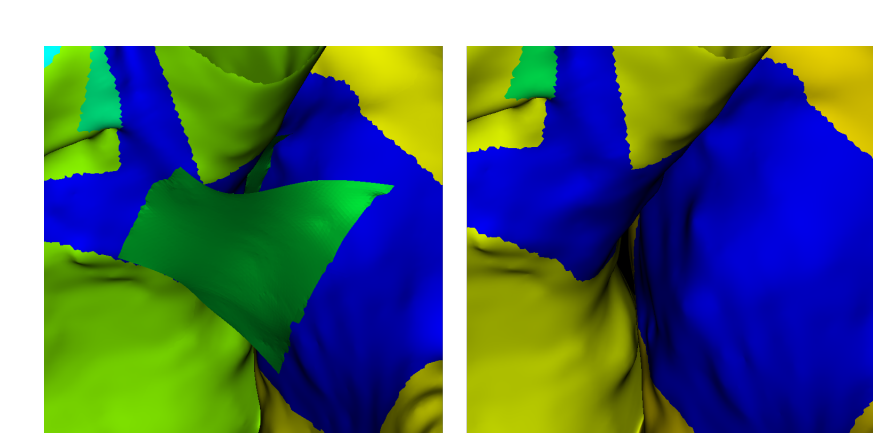
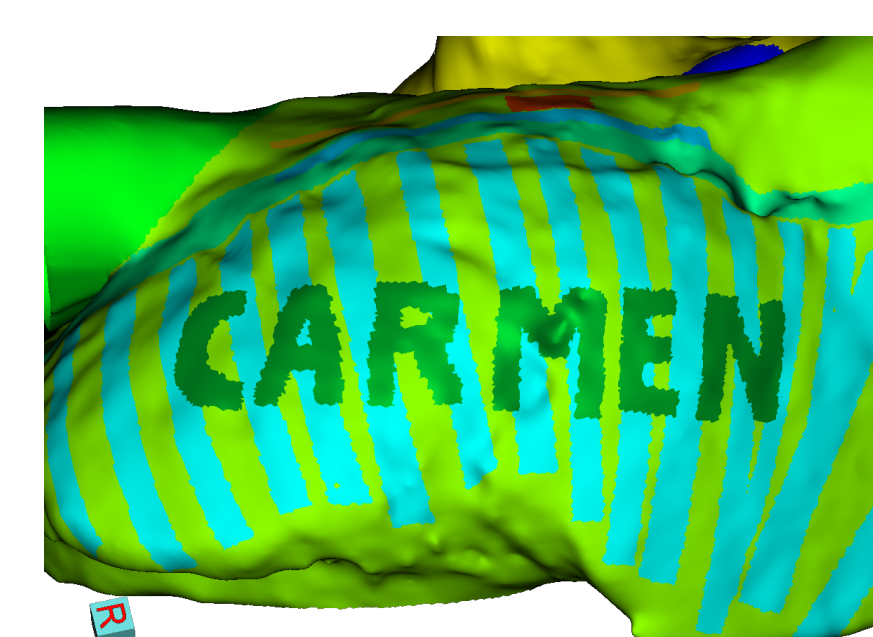


Level-set function as input to MMG3D.

Region selection

Gathers multiple tools to **enrich and modify** a geometry

- selection tools: paint, region, and shape selection
- removal of cells and points
- modify labels and attributes



Future works

CEPS

- P3 finite elements
- bidomain model
- shared memory* parallelism (OpenMP or Intel TBB) for ionic models
- look-up tables to accelerate evaluations of ionic models

MUSIC

- reconstruction of fiber direction
- improve existing toolboxes
- extend visualization interface
- generate customized pipelines
- visualize simulation results